



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142232

TO: James Schultz
Location: REM-2D18&2C18
Art Unit: 1635
Tuesday, January 25, 2005

Case Serial Number: 09163289

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Schultz,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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142232

From: Schultz, James
Sent: Tuesday, January 11, 2005 11:24 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/163,289

Hello,

I need a standard nucleotide sequence search run against SEQ ID NO:3 in the above entitled application. Please include the interference databases.

Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

CRFE

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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[illegible]

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	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
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QY	61 AUCCAUUGACUCCGCGAUGUCUGACCCGUCGAGUUAUUCGCCAAAUUGUGGAGAAUCUGACU 120
Db	61 ATCCATTGCATCCGCGATGTCTGATACCCCTCGATTTCCCAAAATGTGGAGAACTGCAT 120
QY	121 GCAGAAUUGGCGAU 134
Db	121 GCATATTTGTGGT 134
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DEFINITION	Human U1A small nuclear RNA.
ACCESSION	K00788
VERSION	K00788.1 GI:174936
KEYWORDS	U1 small nuclear RNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 165)
TITLE	Branlant,C., Krol,A., Ebel,J.P., Lazare,E., Gallinari,H., Jacob,M., Sri-Widada,J., and Jeanneur,P.
JOURNAL	Nucleotide sequences of nuclear U1A RNAs from chicken, rat and man
MEDLINE	81053758
PUBMED	6159387
REFERENCE	2 (bases 1 to 63; 76 to 98; 111 to 149)
AUTHORS	Lih,W.L. and Pederson,T.
TITLE	Ribonucleoprotein organization of eukaryotic RNA. XXXI. Structure of the U1 small nuclear ribonucleoprotein
JOURNAL	J. Mol. Biol. 180 (4), 947-960 (1984)
MEDLINE	85134903
PUBMED	6084724
REFERENCE	3 (bases 1 to 165)
AUTHORS	Reveillard,I., Lelay-Taha,M.N., Sri-Widada,J., Brunel,C. and Jeanneur,P.
TITLE	Mg2+ induces a sharp and reversible transition in U1 and U2 small nuclear ribonucleoprotein configurations
JOURNAL	Mol. Cell. Biol. 4 (9), 1890-1899 (1984)
MEDLINE	85036342
PUBMED	6238232
COMMENT	The original source text: Human Hela cell URNA.
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RESULT 5	AR424957	203 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	AR424957				
DEFINITION	Sequence 16454 from patent US 6639063.				
Accession	AR424957				

ORIGIN

[illegible]

Query Match	60.5%;	Score 127.6;	DB 6;	Length 203;
Best Local Similarity	73.1%;	Pred. No. 5;	8e-30;	
Matches 98;	Conservative 32;	Mismatches 4;	Indels 0;	Gaps 0;

RESULT 7			
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LOCUS			linear
DEFINITION	EST and encoded human protein.		
Accession	BD120510		

VERSION
 BDJ200210.1.G1:73215420
 KEYWORDS
 JP 2002010789-A:12587.
 SOURCE
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 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 203)
 REFERENCE
 Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
 EST and encoded human protein
 Patent: JP 2002010789-A:12587 15-JAN-2002;
 JOURNAL

COMMENT	
OS	Homo sapiens (human)
PN	JP 2002010789-A/12587
PD	15-JAN-2002
PF	07-AUG-2000 JP 2000280969
PR	05-AUG-1999 US 60/147499
PI	JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE GIORDANO
PC	C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, C12N15/00
CC	EST and encoded human protein
PH	Key Location/Qualifiers

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QY 121 GCAGAAUUGGCGAU 134
Db 121 GCATTAATTGTGTGT 134
RESULT 8
AR424959 231 bp DNA linear PAT 18-DEC-2003
LOCUS AR424959
DEFINITION Sequence 16456 from patent US 6639063.
ACCESSION AR424959
VERSION AR424959.1 GI:40180069
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 231)
AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 16456 28-OCT-2003;
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/mol_type="genomic DNA"
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Best Local Similarity 73.1%; Pred. No. 5.9e-30;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY 1 AUAUCUACGUGGAGGAGAGUACCAUGAUCAGAGUGUUUCCAGGGGAGGCGU 60
Db 1 ATACTTACCTGGGAGGAGATACCATGATCAGAGGTGGTTTCCAGGGGAGGCGT 60
QY 61 AUCCAUUGCAGCUCGCGAGUGUCGACCCCGGAGUUUUCCCAAAUGUGGAGAACTCGACU 120
Db 61 ATCCATTGCACTCCGAGATGTGCTGACCCCTGCGATTCCCAAAATGTGGGAACTCGACT 120
QY 121 GCAGAAUUGGCGAU 134
Db 121 GCATTAATTGTGTGT 134
RESULT 9
AX985653 231 bp DNA linear PAT 15-JAN-2004
LOCUS AX985653
DEFINITION Sequence 16456 from Patent EP104808.
ACCESSION AX985653
VERSION AX985653.1 GI:40991793
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 16456 06-JUN-2001;
FEATURES
source 1..231
Location/Qualifiers
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/organism="Homo sapiens"
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QY 61 AUCCAUUGCAGCUCGCGAGUGUCGACCCCGGAGUUUUCCCAAAUGUGGAGAACTCGACU 120
Db 61 ATCCATTGCACTCCGAGATGTGCTGACCCCTGCGATTCCCAAAATGTGGGAACTCGACT 120
QY 121 GCAGAAUUGGCGAU 134
Db 121 GCATTAATTGTGTGT 134
RESULT 10
BD120512 231 bp DNA linear PAT 18-SEP-2002
LOCUS BD120512
DEFINITION EST and encoded human protein.
ACCESSION BD120512
VERSION BD120512.1 GI:23215422
KEYWORDS JP 2002010789-A/12589
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 231)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.Y.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 12589 15-JAN-2002;
COMMENT
GENSET CORP
OS Homo sapiens (human)
PN JP 2002010789-A/12589
PD 15-JAN-2002
PF 07-AUG-2000 JP 200280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EYE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
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Db 1 AATCTTACCTGGAGGAGATATCATGATCAGAAAGTGTGTTTCCAGGGGAGGCTT 60
Qy 61 AUCCAUUGCAUUCGGAUGUGUCUGACCCUGCGAUUUUCCCAAAUUGGGAACUGGACU 120
Db 61 ATCTTACCTGGAGGAGATATCATGATCAGAAAGTGTGTTTCCAGGGGAGGCTT 120
Qy 121 GCAGAAUUGGCGAU 134
Db 121 GCATTAATTTGTGTG 134

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DEFINITION Human gene possibly encoding UI RNA.
ACCESSION V00587
VERSION V00587.1 GI:36076
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 301)
TITLE Monstein,H.J., Westin,G., Philipson,L. and Petersson,U.
JOURNAL A candidate gene for human UI RNA
MEDLINE EMBO J. 1 (1), 133-137 (1982)
PUBMED 84182447
FEATURES
source 6201353
Location/Qualifiers
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83..246
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Best Local Similarity 73.1%; Pred. No. 5.9e-30;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AUAUCUACCGGAGGAGGAUACCAUAGUAGUGUUUCCAGGGGAGGACU 60
Db 83 ATCTTACCTGGAGGAGATATCATGATCAGAAAGTGTGTTTCCAGGGGAGGCTT 142
Qy 61 AUCCAUUGCAUUCGGAUGUGUCUGACCCUGCGAUUUUCCCAAAUUGGGAACUGGACU 120
Db 143 ATCTTACCTGGAGGAGATATCATGATCAGAAAGTGTGTTTCCAGGGGAGGCTT 202
Qy 121 GCAGAAUUGGCGAU 134
Db 203 GCATTAATTTGTGTG 216

RESULT 12
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LOCUS AR424955 355 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 16452 from patent US 6639063.
ACCESSION AR424955
VERSION AR424955.1 GI:40180065
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 355)
TITLE Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
JOURNAL EST's and encoded human proteins
FEATURES Patent: US 6639063-A 16452 28-OCT-2003;
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Location/Qualifiers
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Db 121 GCATTAATTTGTGTG 134

RESULT 13
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LOCUS AX985649 355 bp DNA linear PAT 15-JAN-2004
DEFINITION Sequence 16452 from Patent EP1104808.
ACCESSION AX985649
VERSION AX985649.1 GI:40991789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1
TITLE Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
JOURNAL ESTs and encoded human proteins
FEATURES Patent: EP 1104808-A 16452 06-JUN-2001;
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DEFINITION EST and encoded human protein.
ACCESSION BD120508
VERSION BD120508.1 GI:23215418
KEYWORDS JP 2002010789-A/12585.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS 1 (bases 1 to 355)
TITLE Edwards,J.B.D.M., Jobert,S. and Giordano,J.B.
EST and encoded human protein

JOURNAL	Patent: JP 2002010789-A 12585 15-JAN-2002;	
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PD	15-JAN-2002	JP 2002280989
PF	07-AUG-2000	JP 2002280989
PR	05-AUG-1999	US 60/147499
PI	JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELLIN JOBERT, JEAN EVE	
GIORDANO		
PC	C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19,	PC
	C12N1/21,	
PC	C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00,	PC
C12N15/00		
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FM	Key	
FT	source	Location/Qualifiers
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ORIGIN		

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Db      108 ATACTTACCTGCGGAGGGGAGATACCAAGATGATGTTTCCCGAGGCGAGGCTT 167
QY      61  AUCCAUUGGACUUCGCGAUGUGUCUGACCCGUCGGAUUNUCCCGAAUAGUGGGGAAACUUCGACU 120
        |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      168 ATCACTTGCACTCCGGGAGTGTCTGACCCCTCGAATTCCCAATGTGGGAAACTCGACT 227
QY      121 GCAGAUUUGCGCAU 134
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Db      228 GCATATATTGTGT 241

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Search completed: January 19, 2005, 17:47:31
Job time : 1518 secs

Search completed: January 19, 2005, 17:47:31
Job time : 1518 secs

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QY	61 AUCCAUTUGCACUCCGAGAGUGUCUGAACCCTTCGCAUUUUCCCCAAAGUGGGAAAACUCGACU	120			
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Db	61 ATCCATTGCACCTCCGAGTAGTGTCAACCCTCGGATTTCCCAAAGTGGGAAACTGCACT	120			
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT	FEATURES
HUMSNUT1C1	Human U1 small nuclear RNA gene, clone cosD1, complete cds.	M28012	M28012.1	U1 small nuclear RNA.	Homo sapiens (human).	Homo sapiens	1	Bernstein, L. B., Manser, T. and Weiner, A. M.	Human U1 small nuclear RNA genes: extensive conservation of flanking sequences suggests cycles of gene amplification and transposition	Mol. Cell. Biol. 5 (9), 2159-2171 (1985)	86284656	3837185	Original source text: Human blood DNA, clone cosD1, location/Qualifiers	source

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          /note="U1 small nuclear RNA; G00-119-560"
ORIGIN

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Query Match          60.5%; Score 127.6; DB 9; Length 362;  
Best Local Similarity 73.1%; Pred. No. 5,9e-30;  
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DB      108 ATACTTAACTGCGCAGGGAGATACCAGATGCACGAAGGTGGTTTCCACAGGCGAGGCTT 167  
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QY      61 AUCCAUUGCACUCCGGAUUGUCUGACCCCUGCCGAUUUCCCCCAAUUGUGGGAACAUCGACU 120  
        |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
DB      168 ATCCATTGCACTCCGGATGTGCTAACCCCTGCGAFTTCCCCAAAATGTGGGAAACTCGACT 227  
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QY      121 GCAGAUUUGCGCAU 134  
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DB      228 GCATAATTGTGTGT 241  
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Search completed: January 19, 2005, 17:47:31  
Job time : 1518 secs
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Search completed: January 19, 2005, 17:47:31
Job time : 1518 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 14:11:14 : Search time 281 Seconds
(without alignments)
3941.736 Million cell updates/sec

Title: US-09-163-289a-3

Perfect score: 211

Sequence: 1 aaacuacucgucgacgggag.....ucguucgcguuucccug 211

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134866 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	205.4	97.3	212	2	AAV32602	AAV32602 Chimeric
2	143.8	68.2	208	12	AD134065	AD134065 N-SMase h
3	127.6	60.5	164	6	ABA92582	ABA92582 U1DNA amp
4	127.6	60.5	746	4	AAK92184	AAK92184 Human cDN
5	127.6	60.5	746	4	AAK93450	AAK93450 Human cDN
6	127.6	60.5	746	12	AD128611	AD128611 5' end of
7	127.6	60.5	746	12	AD129877	AD129877 5' end of
8	127.6	60.5	781	4	AAH07536	AAH07536 Human cDN
9	127.6	60.5	1858	4	AAK94493	AAK94493 Human ful
10	127.6	60.5	1858	12	AD131299	AD131299 Full leng
11	127.6	60.5	1912	5	AAK64548	AAK64548 DNA encod
12	127.6	60.5	1914	4	AAK94440	AAK94440 Human cDN
13	127.6	60.5	1914	12	AD131195	AD131195 Full leng
14	127.6	60.5	1956	4	AAH14832	AAH14832 Human cDN
15	127.6	60.5	118067	12	AD131310	AD131310 Hypermeth
16	127.6	60.5	118067	12	AD131310	AD131310 Hypermeth
17	126	59.7	165	2	AAK93939	AAK93939 UI RNA. 3
18	126	59.7	165	2	AAK94883	AAK94883 Human UI
19	122	57.8	122	2	AAK96717	AAK96717 Human REN
20	121.2	57.4	167	12	ACH84933	ACH84933 Human gen
21	121.2	57.4	515	12	ACH71233	ACH71233 Human gen

22	121.2	57.4	607	10	ADD27745	ADD27745 pGem3z+U
23	119.4	56.6	825	4	AAI95431	AAI95431 Human neu
24	116.8	55.4	164	2	AAO89146	AAO89146 RNA mole
25	116.4	53.2	607	10	ADD27746	ADD27746 pGem3z+U
26	115.8	54.9	909	5	AAK69273	AAK69273 DNA encod
27	115.8	54.9	909	5	AAK69273	AAK69273 DNA encod
28	115.6	54.8	1343	4	AAK80095	AAK80095 Human imm
29	115.6	54.8	1343	4	AAK80094	AAK80094 Human imm
30	115.6	54.8	1354	4	AAK80093	AAK80093 Human imm
31	115.6	54.8	1354	4	AAK80092	AAK80092 Human imm
32	115.6	54.8	1354	4	AAK80092	AAK80092 Human imm
33	115.6	54.8	1354	4	AAK80096	AAK80096 Human imm
34	115.6	54.8	1470	4	AAK80091	AAK80091 Human imm
35	112.2	53.2	4639	6	AAK96552	AAK96552 Human sma
36	111.6	52.9	365	3	AAK32349	AAK32349 Human sec
37	110	52.1	139	3	AAK87354	AAK87354 Rat hepat
38	109.6	51.9	593	12	ACH68354	ACH68354 Human gen
39	109	51.7	607	10	ADD27763	ADD27763 pGem3z+U
40	108	51.2	607	10	ADD27761	ADD27761 pGem3z+U
41	106.8	50.6	607	10	ADD27764	ADD27764 pGem3z+U
42	106.2	50.3	607	10	ADD27762	ADD27762 pGem3z+U
43	104.8	49.7	402	4	AAI88559	AAI88559 Human pol
44	103	48.8	107	3	AAK14652	AAK14652 Human sec
45	102.6	48.6	639	12	AD13089	AD13089 Hypermeth

ALIGNMENTS

RESULT 1	
AAV32602	
ID	AAV32602 standard; RNA; 212 BP.
XX	AAV32602;
AC	
XX	
XX	23-SEP-1998 (first entry)
DT	
XX	
XX	Chimeric UI snRNA.
DE	
XX	Fibrillin mRNA; UI snRNA gene; hammerhead ribozyme loop; growth factor;
KW	alzheimer's disease; huntingdon's disease; hereditary parkinsonism;
KM	toxic peptide; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
FH	
FT	Key
FT	Location/Qualifiers
FT	1
FT	/*tag= a
FT	/note= "Optionally mono- or timethyl-guanosine cap"
FT	15. .17
FT	/*tag= b
FT	/note= "Forms double stranded region with bases 120-122"
FT	19. .49
FT	/*tag= c
FT	50. .93
FT	/*tag= d
FT	94. .119
FT	/*tag= e
FT	121. .124
FT	/*tag= f
FT	/note= "Forms double stranded region with bases 14-16"
FT	131. .144
FT	/*tag= g
FT	/note= "Forms double stranded region with bases 17-30 of
FT	the target mRNA molecule (AAV32603)"
FT	145. .166
FT	/*tag= h
FT	/note= "Hammerhead ribozyme loop"
FT	152. .163
FT	/*tag= i
FT	/function= "Catalytic domain"
FT	167. .181
FT	misc_binding

```
FT FT /*tag= j
FT FT /note= "Forms double stranded region with bases 1-15 of
FT FT the target mRNA molecule (AAV2603) "
FT FT stem_loop
FT FT /tag= k
XX XX
XX XX W09818811-A1.
XX XX 07-MAY-1998.
XX XX
XX XX 31-OCT-1997; 97WO-US019849.
XX XX
XX XX 31-OCT-1996; 96US-00742943.
XX XX
XX XX (UVO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX XX
XX XX Dietz HC;
XX XX
XX XX WPI; 1998-272128/24.
XX XX
XX XX Nucleic acid construct expressing antisense nucleic acid - used for
XX XX suppression of gene expression for treating numerous diseases.
XX XX
XX XX Example 1; Fig 1; 43pp; English.
XX XX
XX XX The present sequence represents a chimeric U1 snRNA molecule which
XX XX comprises of a 5' and 3' end unmodified stem loop structure separated by
XX XX the antisense core sequence. The antisense core sequence would itself
XX XX comprise of the first 15 coding nucleotides of the fibrillin mRNA
XX XX followed by the 22 bp hammerhead ribozyme loop which is followed by
XX XX coding nucleotides 17-30 of the fibrillin mRNA. The whole chimeric snRNA
XX XX molecule is an example of a novel nucleic acid construct for suppressing
XX XX expression of a target gene. In the example given, the target gene was
XX XX the fibrillin gene. The antisense core sequence of the chimeric snRNA
XX XX molecule would basepair with the fibrillin mRNA, thus suppressing its
XX XX translation. The invention claims that such nucleic acid constructs can
XX XX be used for suppressing gene expression in vivo, in vitro and ex vivo.
XX XX The constructs are also claimed to be useful for producing non-human
XX XX knock-out animals. Therefore, the construct may be useful for treating
XX XX Alzheimer's disease, Huntington's disease, hereditary Parkinsonism and
XX XX other inherited diseases. They may also be useful for treating enzymatic
XX XX related disorders, and for reducing expression of growth factors, toxic
XX XX peptides, ligands, receptors or other proteins
XX XX
XX XX Sequence 212 BP; 45 A; 59 C; 60 G; 0 T; 48 U; 0 Other;
SQ
Query Match 97.3%; Score 205.4; DB 2; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.2e-61;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 UUAACUUGGACGAGGAGAUACCAUGAUACGAAAGUGUGUUUCCAGGGCGAGGCUUUAUCC 64
DB 6 UUAACUUGGACGAGGAGAUACCAUGAUACGAAAGUGUGUUUCCAGGGCGAGGCUUUAUCC 65
QY 65 AUGGACUCCGGAUGUGUCUGACCCCGUGAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 124
DB 66 AUGGACUCCGGAUGUGUCUGACCCCGUGAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 125
QY 125 AAUUGGAGAUUUCUACAGACUAGAUAGUCCUGAGAGAGAAAGCCCUUACGACUUAUAGU 184
DB 126 AAUUGGAGAUUUCUACAGACUAGAUAGUCCUGAGAGAGAAAGCCCUUACGACUUAUAGU 185
QY 185 GGGGAGACUGGUGUGCGGCUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 211
DB 186 GGGGAGACUGGUGUGCGGCUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 212
RESULT 2
AD134065
ID AD134065 standard; RNA; 208 BP.
XX
AC AD134065;
XX
```

```
DT 22-APR-2004 (first entry)
XX
XX N-Smase hammerhead ribozyme.
DE
XX
XX ss; ribozyme; N-Smase mRNA; neutral sphingomyelinase inhibition;
XX apoptosis; atherosclerosis; inflammatory disorder; arthritis;
XX osteoarthritis; Crohn's disease; obesity; diabetes; HIV; liver disorder;
XX cirrhosis; excessive cholesterol; renal failure; central nervous system;
XX CNS disorder; depression; schizophrenia; Alzheimer's disease; hammerhead.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH stem_loop 18..48
XX FT /*tag= a
XX FT stem_loop 49..92
XX FT /*tag= b
XX FT stem_loop 93..118
XX FT /*tag= c
XX FT stem_loop 151..162
XX FT /*tag= d
XX FT stem_loop 186..207
XX FT /*tag= e
XX
XX US2004006039-A1.
XX
XX 08-JAN-2004.
XX
XX 27-MAY-2003; 2003US-00446519.
XX
XX 23-OCT-2001; 2001US-0342631P.
XX 23-OCT-2002; 2002US-00279215.
XX
XX (CHAR/) CHATTERJEE S B.
XX
XX Chatterjee SB;
XX
XX WPI; 2004-081746/08.
XX
XX New nucleic acid molecule comprising a ribozyme that is specific for N-
XX Smease mRNA, useful for treating inflammatory disorders such as arthritis,
XX osteoarthritis, Crohn's disease, obesity, diabetes, HIV, or liver
XX disorders.
XX
XX Claim 3; SEQ ID NO 1; 25pp; English.
XX
XX
XX The present sequence represents a nucleic acid molecule comprising a
XX ribozyme that is specific for N-Smase mRNA. The nucleic acid molecule is
XX useful for inhibiting the activity of neutral sphingomyelinase and for
XX reducing apoptosis and atherosclerosis. The molecule and methods are
XX useful for treating inflammatory disorders such as arthritis,
XX osteoarthritis, Crohn's disease, obesity, diabetes, HIV, liver disorders
XX (e.g. cirrhosis), excessive cholesterol levels, renal failure, or central
XX nervous system (CNS) disorders such as depression, schizophrenia or
XX Alzheimer's disease. The present sequence represents the N-Smase
XX hammerhead ribozyme.
XX
XX Sequence 208 BP; 48 A; 54 C; 56 G; 0 T; 50 U; 0 Other;
SQ
Query Match 68.2%; Score 143.8; DB 12; Length 208;
Best Local Similarity 85.6%; Pred. No. 4.7e-40;
Matches 172; Conservative 0; Mismatches 27; Indels 2; Gaps 1;
QY 8 CUGGACGAGGAGAUACCAUGAUACGAAAGUGUGUUUCCAGGGCGAGGCUUUAUCCAUU 67
DB 9 CUGGACGAGGAGAUACCAUGAUACGAAAGUGUGUUUCCAGGGCGAGGCUUUAUCCAUU 68
QY 68 GCACUCCGGAUGUGUCUGACCCCGUGAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 127
DB 69 GGCACCGGAGUUGUGUCUGACCCCGUGAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU 128
QY 128 UGGCAUUCUACAGACUAGAUAGUCCUGAGAGAGAAAGCCCUUACGACUUAUAGUGGG 187
```

DB 129 AUGUCAUAAUUGCCUGAGUCGUGAGAGAAACCUUCUACAGAAAAAGUGGG 188
 QY 188 GGAUUGCGUUGCGGCUUCCC 208
 DB 189 G--CUGCGUUGCGGCUUCCCC 207

RESULT 3

ABA92582

ID ABA92582 standard; DNA; 164 BP.

XX ABA92582;

DT 21-MAR-2002 (first entry)

DE UIDNA amplification product SEQ ID NO:3.

XX Anti-ENA antibody; extractable nuclear antigen; collagen disease;
 KM systemic erythematode; intracellular non-histone soluble protein;
 KM skin toughening; ds.

XX Synthetic.

XX WO200190756-A1.

XX 29-NOV-2001.

XX 21-MAY-2001; 2001WO-0P04251.

XX 26-MAY-2000; 2000JP-00157410.

XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.

XX Murakami A, Kojima K;

XX WPI; 2002-089938/12.

XX Assaying anti-extractable nuclear antigen (ENA) antibody based on
 PT reaction of antigen complex with specimen, applicable in diagnosis of
 PT collagen diseases e.g. systemic erythematodes and skin toughening.

XX Example 1; Page 53; 59pp; Japanese.

XX The present invention describes assaying anti-extractable nuclear antigen
 CC (ENA) antibody recognising an antigen containing a first RNA and a first
 CC intracellular non-histone soluble protein, comprising forming a complex
 CC between a second RNA and a first protein molecule, reacting such complex
 CC with a specimen, and detecting the reaction product. The method is
 CC applicable in the diagnosis of collagen diseases e.g. systemic
 CC erythematodes and skin toughening. The method is convenient and highly
 CC sensitive, which is comparable with the conventional DID method, with
 CC reagents easy to handle and store. The present sequence represents a
 CC UIDNA nucleotide sequence, which is used in an example from the present
 CC invention

XX Sequence 164 BP; 32 A; 42 C; 47 G; 43 T; 0 U; 0 Other;

XX Query Match 60.5%; Score 127.6; DB 6; Length 164;

XX Best Local Similarity 73.1%; Pred. No. 2.1e-34;

XX Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAUCUACCGUGAGGAGAGAUACCAUAGUACGAAAGUGUUTUCCAGGGCGAGGCUU 60

DB 1 AACTTAACCTGGAGGAGAGATACATGATCAGAAAGTGTTTCCAGGGCGAGGCTT 60

QY 61 AUCGAUUGACUUCGCGAGUGUGUGAGCCUGCGAUUUUCCCAAAUUGGAGAAACUGACU 120

DB 61 ATCATTTGACATCTCGGATGTGACCCCTCGCATTTTCCCAAAATGTGGAAACTGACT 120

QY 121 GCAGAAUUGGCGAU 134

DB 121 GCATAATTGTGTGT 134

RESULT 4

AAK92184

ID AAK92184 standard; cDNA; 746 BP.

XX AAK92184;

DT 06-NOV-2001 (first entry)

DE Human cDNA 5'-end sequence, SEQ ID NO: 644.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EPI130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y, H;

XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX Claim 2; SEQ ID NO 644; 1380BP + Sequence Listing; English.

XX The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is the nucleotide sequence of the 5'-end of
 CC a cDNA provided in the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in CD-
 CC ROM format directly from EPO

XX Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;

XX Query Match 60.5%; Score 127.6; DB 4; Length 746;

XX Best Local Similarity 73.1%; Pred. No. 3.6e-34;

XX Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAUCUACCGUGAGGAGAGAUACCAUAGUACGAAAGUGUUTUCCAGGGCGAGGCUU 60

DB 1 AACTTAACCTGGAGGAGAGATACATGATCAGAAAGTGTTTCCAGGGCGAGGCTT 60

QY 61 AUCGAUUGACUUCGCGAGUGUGUGAGCCUGCGAUUUUCCCAAAUUGGAGAAACUGACU 120

DB 61 ATCATTTGACATCTCGGATGTGACCCCTCGCATTTTCCCAAAATGTGGAAACTGACT 120

QY 121 GCAGAAUUGGCGAU 134

DB 121 GCATAATTGTGTGT 134

RESULT 5

AAK93450

ID AAK93450 standard; cDNA; 746 BP.

AC AAK93450;
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human cDNA clone representative sequence, SEQ ID NO: 1910.
DE
XX
XX Human, full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
XX Homo sapiens.
XX
XX EP130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-00114089.
XX
XX 08-JUL-1999; 99JP-00194486.
XX
XX 11-JAN-2000; 2000JP-00118774.
XX
XX 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX
XX Ora T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-524255/58.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
XX Example 11; SEQ ID NO 1910; 1380bp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence was used as the representative sequence
CC from a human clone which was used in homology searches to identify the
CC clone. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in CD-ROM format directly from
CC EPO
XX
SQ Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;
Query Match 60.5%; Score 127.6; DB 4; Length 746;
Best Local Similarity 73.1%; Pred. No. 3.6e-34;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY 1 AUAUCUUAACCCUGGAGGAGAGAUACCAUGACGAGAGUGUUUCCCAAGGCGAGGCUU 60
DB 1 ATACTTACCTGGCAGGAGATACCATGATCAGGAAGTGTTTCCCAAGGCGAGGCTT 60
QY 61 AUCCAUUGCAGUCUGGAGUGUGGAGCCCGUGGAGUUUCCCAAUUGGAGAACTUGACU 120
DB 61 ATCCATTGCACTCCGATGTGCTGACCCCTCGCATTTCCCAATGTGGAAACTGCACT 120
QY 121 GCAGAAUUGGCGAU 134
DB 121 GCATAATTGTGTGT 134
RESULT 6
ADL28611
ID ADL28611 standard; cDNA; 746 BP.
XX
XX ADL28611;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX

DE 5' end of a human cDNA molecule Seqid 644.
XX
XX human; medicine; signal transduction; glycoprotein; transcription;
XX oligo-capping method; ss.
XX
XX Homo sapiens.
XX
XX EP1396543-A2.
XX
XX 10-MAR-2004.
XX
XX 07-JUL-2000; 2003EP-00025638.
XX
XX 08-JUL-1999; 99JP-00194486.
XX
XX 11-JAN-2000; 2000JP-00118774.
XX
XX 02-MAY-2000; 2000JP-00183865.
XX
XX 07-JUL-2000; 2000EP-00114089.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX
XX Ora T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2004-204755/20.
XX
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
XX
XX disclosure; SEQ ID NO 644; 1340bp; English.
XX
XX This invention relates to a novel primers useful for synthesizing full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polynucleotide sequence is the
XX 5' end of a full length human cDNA sequence of the invention.
XX
SQ Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;
Query Match 60.5%; Score 127.6; DB 12; Length 746;
Best Local Similarity 73.1%; Pred. No. 3.6e-34;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY 1 AUAUCUUAACCCUGGAGGAGAGAUACCAUGACGAGAGUGUUUCCCAAGGCGAGGCUU 60
DB 1 ATACTTACCTGGCAGGAGATACCATGATCAGGAAGTGTTTCCCAAGGCGAGGCTT 60
QY 61 AUCCAUUGCAGUCUGGAGUGUGGAGCCCGUGGAGUUUCCCAAUUGGAGAACTUGACU 120
DB 61 ATCCATTGCACTCCGATGTGCTGACCCCTCGCATTTCCCAATGTGGAAACTGCACT 120
QY 121 GCAGAAUUGGCGAU 134
DB 121 GCATAATTGTGTGT 134
RESULT 7
ADL29877
ID ADL29877 standard; cDNA; 746 BP.
XX
XX ADL29877;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX 5' end of a representative human cDNA cluster Seqid 1910.
XX
XX human; medicine; signal transduction; glycoprotein; transcription;
XX oligo-capping method; ss.
XX
XX Homo sapiens.
OS

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XX  EP1396543-A2.
XX  10-MAR-2004.
XX  07-JUL-2000; 2003EP-00025638.
XX  08-JUL-1999; 99JP-00194486.
XX  11-JAN-2000; 2000JP-00118774.
XX  02-MAY-2000; 2000JP-00183865.
XX  07-JUL-2000; 2000EP-00114089.
XX  (REAS-) RES ASSOC BIOTECHNOLOGY.
XX  Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX  Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX  WPI; 2004-204755/20.
XX  New oligonucleotide primers (830 CDNAs) useful for synthesizing full
XX  length human cDNAs.
XX  Example 18; SEQ ID NO 1910; 1340bp; English.
XX  This invention relates to a novel primers useful for synthesizing full
XX  length cDNA molecules that encode human proteins. Specifically, it refers
XX  to secretory or membrane proteins that are potential therapeutic agents/
XX  target molecules in the field of medicine, and in particular genes
XX  encoding proteins that are associated with signal transduction,
XX  glycoproteins and transcription. The present invention describes a method
XX  for efficiently cloning a full length human cDNA from both the 5' and 3'
XX  ends using the oligo-capping method. This polynucleotide sequence is the
XX  5' end of a representative human DNA cluster of the invention.
XX  Sequence 746 BP; 201 A; 194 C; 181 G; 165 T; 0 U; 5 Other;
XX  Query Match 60.5%; Score 127.6; DB 12; Length 746;
XX  Best Local Similarity 73.1%; Pred. No. 3.6e-34;
XX  Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY  1 AUAUUUACCGGAGGAGAGUACAUUACGAGAGUGUUUUCCAGGCGGAGGCUU 60
DB  1 AATCTTACCTGGCAGGAGAGATACATGATCAGAGAGTGTTTCCAGGGGAGGCTT 60
QY  61 AUCCAUUGACUCCGAGUGUGUACCCCGGAGUUUUCCCAAUUGGGGAAACUCGACU 120
DB  61 ATCCATTGACATCCGGATGCTGACCCCTGCGATTTCCTCCAAATGTGGGAACTCGACT 120
QY  121 GCAGAAUUGGCGAU 134
DB  121 GCATAATTGTGTGT 134
XX  RESULT 8
XX  ID AAH07536 standard; cDNA; 781 BP.
XX  AAH07536;
XX  26-JUN-2001 (first entry)
XX  Human cDNA clone (5'-primer) SEQ ID NO:4371.
XX  Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX  Homo sapiens.
XX  EP1074617-A2.
XX  07-FEB-2001.
XX  28-JUL-2000; 2000EP-00116126.

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PR  29-JUL-1999; 99JP-00248036.
PR  27-AUG-1999; 99JP-00300253.
PR  11-JUN-2000; 2000JP-00118775.
PR  02-MAY-2000; 2000JP-00183767.
PR  09-JUN-2000; 2000JP-00241899.
XX  (HELIX-) HELIX RES INST.
XX  Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX  Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX  WPI; 2001-318749/34.
XX  Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX  length cDNAs defined in the specification, and for the detection and/or
XX  diagnosis of the abnormality of the proteins encoded by the full-length
XX  cDNAs.
XX  Claim 1; SEQ ID NO 4371; 2537pp + Sequence listing; English.
XX  The present invention describes primer sets for synthesizing 5602 full-
XX  length cDNAs defined in the specification. Where a primer set comprises:
XX  (a) an oligo-dT primer and an oligonucleotide complementary to the
XX  complementary strand of a polynucleotide which comprises one of the 5602
XX  nucleotide sequences defined in the specification, where the
XX  oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX  of an oligonucleotide comprising a sequence complementary to the
XX  complementary strand of a polynucleotide which comprises a 5'-end
XX  sequence and an oligonucleotide comprising a sequence complementary to a
XX  polynucleotide which comprises a 3'-end sequence, where the
XX  oligonucleotide comprises at least 15 nucleotides and the combination of
XX  the 5'-end sequence/3'-end sequence is selected from those defined in the
XX  specification. The primer sets can be used in antisense therapy and in
XX  gene therapy. The primers are useful for synthesizing polynucleotides,
XX  particularly full-length cDNAs. The primers are also useful for the
XX  detection and/or diagnosis of the abnormality of the proteins encoded by
XX  the full-length cDNAs. The primers allow obtaining of the full-length
XX  cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX  AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
XX  represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX  oligonucleotides, all of which are used in the exemplification of the
XX  present invention
XX  Sequence 781 BP; 168 A; 248 C; 207 G; 148 T; 0 U; 10 Other;
XX  Query Match 60.5%; Score 127.6; DB 4; Length 781;
XX  Best Local Similarity 73.1%; Pred. No. 3.7e-34;
XX  Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY  1 AUAUUUACCGGAGGAGAGUACAUUACGAGAGUGUUUUCCAGGCGGAGGCUU 60
DB  1 AATCTTACCTGGCAGGAGAGATACATGATCAGAGAGTGTTTCCAGGGGAGGCTT 60
QY  61 AUCCAUUGACUCCGAGUGUGUACCCCGGAGUUUUCCCAAUUGGGGAAACUCGACU 120
DB  61 ATCCATTGACATCCGGATGCTGACCCCTGCGATTTCCTCCAAATGTGGGAACTCGACT 120
QY  121 GCAGAAUUGGCGAU 134
DB  121 GCATAATTGTGTGT 134
XX  RESULT 9
XX  ID AAH94493 standard; cDNA; 1858 BP.
XX  AAH94493;
XX  06-NOV-2001 (first entry)
XX  Human full-length cDNA, SEQ ID NO: 3332.
XX  Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

```

	XX	Homo sapiens.
OS	XX	EPII30094-A2.
PX	XX	05-SEP--2001.
PP	XX	07-JUL--2000; 2000EP-00114089.
PR	XX	08-JUL--1999; 99JP-00194486.
PM	XX	11-JAN--2000; 2000JP-00118774.
PN	XX	02-MAY--2000; 2000JP-00183765.
PA	XX	(HELI-) HELIX RES INST.
PI	XX	Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y,
PT	XX	Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,
DR	XX	WPI: 2001-524255/58.
DN	XX	P-PSTDB; AAA93561.
PS	XX	Claim 8; SEQ ID NO 3332; 1380pp + Sequence Listing; English.
CC	XX	The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
SQ	XX	Sequence 1858 BP; 536 A; 482 C; 399 G; 441 T; 0 U; 0 Other;
Query Match	60.5%; Score 127.6; DB 4; Length 1858;	
Best Local Similarity	73.1%; Pred.No.5.1e-34;	
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0		
Db	1 AUACUUAACCUGGCAGGGAGAUVACAAGGAGUGUUUCGAGGCCAUGCCTT 1 ATACTTAATCCTCGCAAGGAGATAACATCATCACGAAGTGTTTCACAGGCCAAGCCTT	60
Gy	61 AUCCAUGUCCAGCCGAAUGUGUCAACCCCUGAGAUUUCCCCAAUUGUGAAAUCGACU 61 ATCCATTGTGCATCCGGATGTCTGACCCCTGGGATTTCCCAAATGTGGAAAACTCGACT	120
Bd	121 GCAGAAUUGGCGAU 134 121 GCATTAATTTGTGTG 134	
RSLUT 10		
ID ADLJ1299 standard; cDNA; 1858 BP.		
ADLJ1299;		
DT 20-MAY--2004 (first entry)		
DE Full length human cDNA clone SegID 3332.		
KW human; medicine; signal transduction; glycoprotein; transcription; KW oligo-capping method; ss; gene. OS Homo sapiens.		

```

PN      EP1396543-A2.
XX
XX      10-MAR-2004.
XX
XX      07-JUL-2000; 2003EP-00025638.
XX
XX      08-JUL-1999; 99JP-00194486.
XX      PR 11-JAN-2000; 2000JP-00118774.
XX      PR 02-MAY-2000; 2000JP-00183865.
XX      PR 07-JUL-2000; 2000EP-00114089.
XX
XX      (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI      Ota T, Nishikawa T, Isegai T, Hayashi K, Ichii S, Kawat Y,
PI      Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX      WPI, 2004-204755/20.
XX      P-PsDB; ADL31300.
XX
XX      New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX      length human cDNAs.
XX
XX      Example 1; SEQ ID NO 3332; 1340pp; English.
XX
XX      This invention relates to a novel primers useful for synthesizing full
XX      length cDNA molecules that encode human proteins. Specifically, it refers
XX      to secretory or membrane proteins that are potential therapeutic agents/
XX      target molecules in the field of medicine, and in particular genes
XX      encoding proteins that are associated with signal transduction,
XX      glycoproteins and transcription. The present invention describes a method
XX      for efficiently cloning a full length human cDNA from both the 5' and 3'
XX      ends using the oligo-capping method. This polynucleotide sequence is a
XX      full length human cDNA clone of the invention.
XX
XX      SEQ
XX      Sequence 1858 BP; 536 A; 482 C; 399 G; 441 T; 0 U; 0 Other;
XX
XX      Query Match 60.5%; Score 127.6; DB 12; Length 1858;
XX      Best Local Similarity 73.1%; Pred. No. 5.1e-34;
XX      Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
XX
XX      1 AUACUUAACUUGGACAGGAGGAUACCAUGAUUACGAAAGGUGUGUUNUCCAGAGGCGAGGCU 60
XX      1 ATACTTACTCTGGCAGGGAGAGTACCAGTATCAACAAGGTGTTTCCAGAGGCGAGGCTT 60
XX
XX      61 AUCCAUUGCACUCCGGAUUGUCUGAACCCUUGCGAUUUUCCCAAAUUGUGGAAACUCCAGU 120
XX      61 ATCCATTGCACTCCGGAATGTCTGACCCCTCGATTCCCAAAATGTGGGAAACTCGACT 120
XX
XX      121 GCAGAUUUGGCGCAU 134
XX      121 GCATATATTGTGGT 134
XX
XX      Db
XX
XX      RESULT 11
XX      AAS64548/c
XX      ID AAS64548 standard; cDNA; 1912 BP.
XX
XX      AAS64548;
XX      AC
XX      AA64548;
XX
XX      13-FEB-2002 (first entry)
XX
XX      DNA encoding novel human diagnostic protein #352.
XX
XX      Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX      food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX      Homo sapiens.
XX
XX      WO200175067-A2.
XX
XX      11-OCT-2001.
XX
XX      30-MAR-2001; 2001WO-US008631.
XX      Pf

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PR	31-MAR-2000;	2000US-00540217.
PR	23-AUG-2000;	2000US-00649167.
PA	(HYSE-) HYSEQ INC.	
PI	Drimnac RT, Liu C, Tang YT;	
PI	WPI, 2001-639362/73.	
DR	P-PSDB; AEG00361.	
XX	New isolated polynucleotide and encoded polypeptides, useful in	
XX	diagnostics, forensics, gene mapping, identification of mutations	
XX	responsible for genetic disorders or other traits and to assess	
XX	biodiversity.	
PS	Claim 1; SEQ ID NO 352; 103bp; English.	
XX	The invention relates to isolated polynucleotide (I) and polypeptide (II)	
XX	sequences. (I) is useful as hybridisation probes, polymerase chain	
XX	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,	
XX	and in recombinant production of (II). The polynucleotides are also used	
XX	in diagnostics as expressed sequence tags for identifying expressed	
XX	genes. (I) is useful in gene therapy techniques to restore normal	
XX	activity of (II) or to treat disease states involving (II). (II) is	
XX	useful for generating antibodies against it, detecting or quantitating a	
XX	polypeptide in tissue, as molecular weight markers and as a food	
XX	supplement. (II) and its binding partners are useful in medical imaging	
XX	of sites expressing (II). (I) and (II) are useful for treating disorders	
XX	involving aberrant protein expression or biological activity. The	
XX	polypeptide and polynucleotide sequences have applications in	
XX	diagnostics, forensics, gene mapping, identification of mutations	
XX	responsible for genetic disorders or other traits to assess biodiversity	
XX	and to produce other types of data and products dependent on DNA and	
XX	amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic	
XX	coding sequences of the invention. Note: The sequence data for this	
XX	parent did not appear in the printed specification, but was obtained in	
XX	electronic format directly from WIPO at	
XX	ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence 1912 BP; 520 A; 521 C; 547 G; 321 T; 0 U; 3 Other;	
XX		
XX	Query Match	60.5%; Score 127.6; DB 5; Length 1912;
XX	Best Local Similarity	73.1%; Pred. No. 5.2e-34;
XX	Matches	98; Conservative 32; Mismatches 4; Indels 0; Gaps 0.
QY	1	AUACUACCCUGGACAGGGAGAUACCAUGACGAAAGUGGUTUCCACAGGGCGAGGCU 60
DB	146	ATACTTACTCTGGCAGAGGAGATACCATATATTCAGAAAGGAGTTCCTCCAGGGCGAGGCTT 87
QY	61	AUCCAUUGCACUCGCGAGUGUGUCGACCCGUCGCAUUTUCCCAUAUGUGGAAACUCGACU 120
DB	86	ATCATCTGCATCCGCGATGTGTGACCCCTGGGATTTCCCAATGTGGAAACTGACT 27
QY	121	GCAGAAUUGCGCAU 134
DB	26	GCATATATTGTGCT 13
XX	RESULT 12	
XX	AAK94440	
XX	AAK94440 standard; cDNA, 1914 BP.	
XX	AAK94440;	
XX	07-NOV-2001 (first entry)	
XX	Human cDNA, SEQ ID NO: 3228.	
XX	Human; full length cDNA; cDNA synthesis; oligo-capping; 68.	
XX	Homo sapiens.	

XX	FN	EP1130094-A2.
XX	PD	05-SEP-2001.
XX	PF	07-JUL-2000; 2000EP-00114089.
XX	PR	08-JUL-1999; 99JP-00194486.
XX	PR	11-JAN-2000; 2000JP-00118774.
XX	PR	02-MAY-2000; 2000JP-00183765.
XX	PA	(HELI-) HELIX RES INST.
XX	PI	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX	PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX	XX	WI; 2001-524255/58.
XX	DR	P-PSDB; AAM93510.
XX	PT	830 Primers useful for synthesizing full length cDNA clones and their use
XX	PT	in genetic manipulation.
XX	PS	Disclosure; SEQ ID NO 3228; 1380bp + Sequence Listing; English.
XX	XX	The invention relates to primers for synthesizing full length cDNA
XX	CC	clones. 830 cDNA molecules encoding a human protein have been isolated
XX	CC	and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX	CC	been determined. Primers for synthesizing the full length cDNA are useful
XX	CC	for clarifying the function of the protein encoded by the cDNA. The full
XX	CC	length clones were obtained by construction of full length enriched cDNA
XX	CC	libraries that were synthesized by the oligo-capping method. The primers
XX	CC	enable the production of the full length cDNA easily without any special
XX	CC	methods. The present sequence is a human cDNA provided in the
XX	CC	specification. Note: The sequence data for this patent did not form part
XX	CC	of the printed specification, but was obtained in CD-ROM format directly
XX	CC	from EPO
XX	XX	Sequence 1914 BP; 554 A; 501 C; 400 G; 459 T; 0 U; 0 Other;
XX	SO	
XX	XX	Query Match 60.5%; Score 127.6; DB 4; Length 1914;
XX	XX	Best Local Similarity 73.1%; Pred. No. 5.2e-34;
XX	XX	Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0.
XX	QY	1 AUAUCUUAACCCUGGAGGAGUAACCAUGAUUACGAAGUGUGUUUCCAGGGCGAGGCUU 60
XX	DB	3 ATACTTACCTGGGAGGAGGAGATACCATGATCAGCAAGGTGGTTTCCAGGGCGAGGCTT 62
XX	QY	61 AUCGAUUGGACUUCGGAUGUGUGUGACCCUGGCGAUUUUCCCAAAUUGUGGAAACUCGACU 120
XX	DB	63 ATCCATTGCACTCCGGAGATGCTCTACCCCTCGATTCCCAATGTGGGAACTCGACT 122
XX	QY	121 GCAGAUUUGGCGAU 134
XX	DB	123 GCATTAATTGTGGT 136
XX	RESULT 13	
XX	ADL31195	ADL31195 standard; cDNA; 1914 BP.
XX	ADJ31195;	
XX	DT	20-MAY-2004 (first entry)
XX	DE	Full length human cDNA clone segid 3228.
XX	XX	human; medicine; signal transduction; glycoprotein; transcription;
XX	XX	oligo-capping method; ss; gene.
XX	OS	Homo sapiens.
XX	XX	EP1396543-A2.
XX	PD	10-MAR-2004.

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XX 07-JUN-2000; 2003EP-00025638.
PF 08-JUN-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
XX 07-JUN-2000; 2000EP-00114089.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H,
XX WPI; 2004-204755/20.
DR P-PSDB; ADL31196.
XX
PT New oligonucleotide primers (830 CDNAs) useful for synthesizing full
XX length human cDNAs.
PS Example 1; SEQ ID NO 3228; 1340bp; English.
XX
CC This invention relates to a novel primers useful for synthesizing full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polynucleotide sequence is a
XX full length human cDNA clone of the invention.
SQ Sequence 1914 BP; 554 A; 501 C; 400 G; 459 T; 0 U; 0 Other;
Query Match 60.5%; Score 127.6; DB 12; Length 1914;
Best Local Similarity 73.1%; Pred. No. 5,2e-34;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY 1 AUAUCUACCCUGGCGAGGAGAUACCAUAGUACGAGGUGUUUCCAGGCGAGGCTU 60
DB 3 ATACTTAACCTGGCGAGGAGATACCATGATCAGAGAGTGTGTTTCCAGGCGAGGCTT 62
QY 61 AUCCAUUGGACUCGCGAGUGUGUGACCCGCGAUUCCCAAAUGUGGAGAAUCUGACU 120
DB 63 ATCCATTGCACTCCGAGTGTCTGACCCCTGCGATTTCCTCCAAATGTGGGAAACTCGACT 122
QY 121 GCAGAAUUGGCGAU 134
DB 123 GCATAATTGTGTGT 136
RESULT 14
AAH14832
ID AAH14832 standard; cDNA; 1956 BP.
XX
AC AAH14832;
XX
XX 26-JUN-2001 (first entry)
DT 26-JUN-2001 (first entry)
DE Human cDNA sequence SEQ ID NO:12648.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.

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PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T,
XX WPI; 2001-318749/34.
XX
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 12648; 2537bp + Sequence listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH1633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
XX present invention.
SQ Sequence 1956 BP; 377 A; 632 C; 547 G; 400 T; 0 U; 0 Other;
Query Match 60.5%; Score 127.6; DB 4; Length 1956;
Best Local Similarity 73.1%; Pred. No. 5,2e-34;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
QY 1 AUAUCUACCCUGGCGAGGAGAUACCAUAGUACGAGGUGUUUCCAGGCGAGGCTU 60
DB 1 ATACTTAACCTGGCGAGGAGATACCATGATCAGAGAGTGTGTTTCCAGGCGAGGCTT 60
QY 61 AUCCAUUGGACUCGCGAGUGUGUGACCCGCGAUUCCCAAAUGUGGAGAAUCUGACU 120
DB 61 ATCCATTGCACTCCGAGTGTCTGACCCCTGCGATTTCCTCCAAATGTGGGAAACTCGACT 120
QY 121 GCAGAAUUGGCGAU 134
DB 121 GCATAATTGTGTGT 134
RESULT 15
ADF13110
ID ADF13110 standard; DNA; 118067 BP.
XX
AC ADF13110;
XX
XX 12-FEB-2004 (first entry)
DT 12-FEB-2004 (first entry)
DE Hypermethylation site in human breast cancer CpG island locus HBC-37.
XX
XX DNA methylation; CpG dinucleotide rich region;
XX differential methylation hybridisation; DMH; CpG island; screening array;
XX breast cancer; prostate cancer; colon cancer; lung cancer; liver cancer;
XX ovarian cancer; human; HBC; hypermethylation in breast cancer; ds.

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XX Homo sapiens.
 OS
 XX
 PN US2003129602-A1.
 XX
 PD 10-JUL-2003.
 XX
 PF 21-FEB-2002; 2002US-00081327.
 XX
 PR 05-FEB-1999; 99US-0118760P.
 PR 18-FEB-1999; 99US-0120592P.
 PR 04-FEB-2000; 2000US-00497855.
 XX
 PA (HUAN/) HUANG T H.
 XX
 PI Huang TH;
 XX
 DR WPI; 2004-031298/03.
 XX
 PT Differential methylation hybridization assay for detecting
 PT hypermethylation of CpG dinucleotide rich regions in genomic DNA is
 PT useful to diagnose and monitor breast, prostate, colon, lung, liver and
 PT ovarian cancer.
 XX
 PS Claim 17; SEQ ID NO 32; 32pp; English.
 XX
 CC The present invention relates to a method of detecting DNA methylation of
 CC a CpG dinucleotide rich region of a nucleic acid. The method comprises
 CC hybridization by differential methylation hybridization (DMH) in which
 CC the nucleic acid is digested into fragments in which CpG islands are
 CC preserved, attaching the fragments to linker primers, digesting the
 CC linker primer products to digest unmethylated CpG sequences, amplifying
 CC and labelling the remaining linker primer products and detecting labelled
 CC amplicons. Also disclosed is a screening array comprising nucleic acid
 CC fragments fixed to a solid support where each fragment is a CpG
 CC dinucleotide rich fragment comprising at least 200 nucleotides of which
 CC at least 50% are guanine and cytosine. Nucleic acid probes prepared from
 CC a cell sample are used to screen CpG dinucleotide rich fragments fixed
 CC onto a screening array. The invention is useful to diagnose and monitor
 CC prognosis of a disease associated with aberrant DNA methylation,
 CC particularly breast, prostate, colon, lung, liver or ovarian cancer,
 CC especially breast cancer. The present sequence represents the site of
 CC hypermethylation in human breast cancer at a CpG island locus (HBC,
 CC hypermethylation in breast cancer).
 XX
 SQ Sequence 118067 BP; 28717 A; 29403 C; 28733 G; 31214 T; 0 U; 0 Other;
 Query Match 60.5%; Score 127.6; DB 12; Length 118067;
 Best Local Similarity 73.1%; Pred. No. 2.4e-33;
 Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AUAUACUACGCGGAGGAGAUACAUGAUACAGAAAGUGUUUCCAGAGGCGAGGCUU 60
 Db 59420 ATACTTACTCGGAGGAGGAGATGATCAATGATCAAGAAAGTGTTTCCAGAGGCGAGGCTT 59479
 QY 61 AUCCAUUGCAUCCGCGAUGUGUGUACCCUCCGCAUUTCCCAAAUUGGGAAACUCGACU 120
 Db 59480 ATCCATTGCACTCCGATGCTGACCCCGCATTTCCCAATATGCGGAAACTCGACT 59539
 QY 121 GCAGAAUUGGCGAU 134
 Db 59540 GCATTAATTGTGTGT 59553

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OM nucleic - nucleic search, using SW model

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Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	160.8	76.2	215	US-08-724-354D-26 Sequence 26, Appl
2	160.8	76.2	215	US-09-270-984A-26 Sequence 26, Appl
3	127.6	60.5	203	US-09-621-976-16454 Sequence 16454, A
4	127.6	60.5	231	US-09-621-976-16456 Sequence 16456, A
5	127.6	60.5	355	US-09-621-976-16452 Sequence 16452, A
6	127.6	60.5	118067	US-09-497-855A-32 Sequence 32, Appl
7	127.2	60.3	204	US-09-621-976-16458 Sequence 16458, A
8	126	59.7	189	US-09-621-976-16457 Sequence 16457, A
9	126	59.7	207	US-09-621-976-16455 Sequence 16455, A
10	123.2	58.4	175	US-09-621-976-16453 Sequence 16453, A
11	116.8	55.4	164	US-08-704-170-75 Sequence 75, Appl
12	116.8	55.4	164	PCT-US94-02631-75 Sequence 75, Appl
13	111.6	52.9	365	US-09-513-999C-36424 Sequence 36424, A
14	103.2	48.9	157	US-09-621-976-10271 Sequence 10271, A
15	103	48.8	107	US-09-513-999C-18727 Sequence 18727, A
16	102.6	48.6	639	US-09-497-855A-11 Sequence 11, Appl
17	98.6	46.7	5227	US-09-919-172-79 Sequence 79, Appl
18	98.6	46.7	5228	US-09-919-039-216 Sequence 216, Appl
19	98.2	46.5	1121	US-09-919-172-88 Sequence 88, Appl
20	98.2	46.5	1121	US-09-976-594-848 Sequence 848, Appl
21	95	45.0	179	US-08-781-6208-2 Sequence 2, Appl
22	95	45.0	435	US-08-781-6208-3 Sequence 3, Appl
23	91.8	43.5	434	US-08-781-6208-22 Sequence 22, Appl
24	67.4	31.9	3001	US-09-539-333D-171 Sequence 171, Appl
25	61.8	29.3	133	US-09-513-999C-13542 Sequence 13542, A
26	55	26.1	55	US-08-742-943-1 Sequence 1, Appl
27	55	26.1	55	US-08-742-943-2 Sequence 2, Appl

28	54.4	25.8	826	US-09-919-172-99 Sequence 99, Appl
29	54.4	25.8	826	US-09-976-594-811 Sequence 811, Appl
30	36.8	17.4	148	US-09-513-999C-10581 Sequence 10581, A
31	31.6	15.0	83	US-08-862-337-2 Sequence 2, Appl
32	31	14.7	31	US-08-571-986-16 Sequence 16, Appl
33	30.8	14.6	40	US-08-324-362-4 Sequence 4, Appl
34	30.8	14.6	40	US-08-324-362-5 Sequence 5, Appl
35	30.8	14.6	70	US-09-276-533A-3 Sequence 3, Appl
36	30.8	14.6	70	US-09-276-533A-4 Sequence 4, Appl
37	30.8	14.6	70	US-10-158-735-3 Sequence 3, Appl
38	30.8	14.6	70	US-10-158-735-4 Sequence 4, Appl
39	30.6	14.5	1100	US-09-918-686-18 Sequence 18, Appl
40	30.6	14.5	51719	US-09-918-686-2 Sequence 2, Appl
41	30.6	14.5	92139	US-09-918-686-1 Sequence 1, Appl
42	30.2	14.3	92	US-08-464-073-26 Sequence 26, Appl
43	30.2	14.3	92	US-08-428-252-26 Sequence 26, Appl
44	30	14.2	2508	US-09-489-039A-1569 Sequence 1569, Appl
45	29.8	14.1	47	US-08-695-191-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-724-354D-26
Sequence 26, Application US/08724354D
Patent No. 5994119
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PasteSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic RNA
US-08-724-354D-26
Query Match
Best Local Similarity 90.7%; Score 160.8; DB 2; Length 215;
Matches 194; Conservative 0; Mismatches 17; Indels 3; Gaps 2;
QY 1 AUAUACUCCUGCAGGAGGAUACCAUGAUCGAGAGUGUGUUUCCAGGCGAGGAGCU 60
DB 2 AUAUACUCCUGCAGGAGGAUACCAUGAUCGAGAGUGUGUUUCCAGGCGAGGAGCU 61

QY 61 A U C C A U U G C A C U C C G G A U U G C U G A C C C C U G G A U U U C C C A A A U U G G G A A C U C G A C U 120

Db 62 A U C C A U U G C A C U C C G G A U U G U G C U G A C C C C U G G A U U U C C C A A A U U G G G A A C U C G A C U 121

QY 121 G C A G A U U U G G C G - A U C U C C A G C A C U G A U U G A U U C C U G A G A G A A A C G C C C U C G A C - G C 177

Db 122 G C A G A U U U G U U U A C A C U C C A C A G C U G A U A G U C C G G A G A G A C A A A C U G U C U C C C C A G 181

QY 178 A U C U A U G G G G G A C U G C G U U G C G C G C U U U C C C U G 211

Db 182 G C C U A U G G G G G A C U G C G U U C C G C G C U U U C C C C U G 215

```

1 RESULT 2
2 US-09-270-984A-26
3 ; Sequence 26, Application US/09270984A
4 ; Patent No. 6048965
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Dietz, Harry C.
7 ; TITLE OF INVENTION: MAMMALIAN REGULATOR OF
8 ; TITLE OF INVENTION: NONSENSE-MEDIATED RNA DECAY
9 ; NUMBER OF SEQUENCES: 29
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Fish & Richardson, P.C.
12 ; STREET: 4225 Excutive Square, Suite 1400
13 ; CITY: La Jolla
14 ; STATE: CA
15 ; COUNTRY: USA
16 ; ZIP: 92037
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Diskette
19 ; COMPUTER: IBM Compatible
20 ; OPERATING SYSTEM: Windows95
21 ; SOFTWARE: FastSeq for Windows Version 2.0
22 ; CURRENT APPLICATION DATA:
23 ; APPLICATION NUMBER: US/09/270,984A
24 ; FILING DATE:
25 ; PRIOR APPLICATION DATA:
26 ; APPLICATION NUMBER: 08/724,354
27 ; FILING DATE:
28 ; ATTORNEY/AGENT INFORMATION:
29 ; NAME: Haile, Lisa A.
30 ; REGISTRATION NUMBER: 38,347
31 ; REFERENCE/DOCKET NUMBER: 07265/090001
32 ; TELECOMMUNICATION INFORMATION:
33 ; TELEPHONE: 619-678-5070
34 ; TELEFAX: 619-678-5099
35 ; INFORMATION FOR SEQ ID NO: 26:
36 ; SEQUENCE CHARACTERISTICS:
37 ; LENGTH: 215 base pairs
38 ; TYPE: nucleic acid
39 ; STRANDEDNESS: single
40 ; TOPOLOGY: linear
41 ; MOLECULE TYPE: genomic RNA
42 ; IS-09-270-984A-26

```

Query March	76.2%	Score 160.8;	DB 3;	Length 215;
Best Local Similarity	90.7%	Pred. No. 4e-49;		
Matches 194; Conservative	0;	Mismatches 17;	Indels 3;	Gaps 2;

QY	1	AUAUUUACUUGGCAAGGGAGAGUACCAUAUATCCAGAAAGUGUUNUCCAGAGGCGAGAGCU	60
Db	2	AUAUUUACUUGGCAAGGGAGAGUACCAUAUATCCAGAAAGUGUUNUCCAGAGGCGAGAGCU	61
QY	61	AUUCAUUUGACUUCGCGAGUUGUCUGAAGCCUUCGAGUUNUCCCAAAAGUGGAGAAACUAGACU	120
Db	62	AUUCAUUUGACUUCGCGAGUUGUCUGAAGCCUUCGAGUUNUCCCAAAAGUGGAGAAACUAGACU	121
QY	121	GCAGAAUUGGCG-AUUCUCACAGACUAGUAGUCUGGAGAGAGAAAGCCUUCGAC-AGC	177
Db	122	GCAAAAUUUGUUGAGACUUCGAGUCUAGUAGUUCUGGAGAGAGAAACUGUUCUCCCCAGAG	181

Qy 178 AUTCAGUGGGGACUCGCGUUGCGGCUUCCCCUG 211
|||
Db 182 GGCUAUGGGGACUCGCGUUGCGGCUUCCCCUG 215

```

RESULT 3
US-09-621-976-16454
/ Sequence 16454, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OR INVENTION: ESTs and Encoded Human Proteins
/ FILE REFERENCE: GENSET, 054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 16454
/ LENGTH: 203
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-621-976-16454

```

Query Match	60.5%	Score 127.6;	DB 4;	Length 203;
Best Local Similarity	73.1%	Pred. NO. 5.3e-37;		
Matches 98; Conservative	32;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

```

RESULT: 4
US-09-621-976-16456
; Sequence 16456, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTY and Encoded Human Proteins
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ. ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ. ID NO. 16456
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16456

```

Query Match	60.5%	Score 127.6;	DB 4;	Length 231;
Best Local Similarity	73.1%;	Pred. No. 5,7e-37;		
Matches 98;	Conservative 32;	Mismatches 4;	Indels 0;	Gaps 0;

QY 1 AUAUUACUCCUGGACAGGGAGAUACCAUGAUACGAGAAGUGUUNUCCACAGGGGAGGUCU 60
Db 1 AUAUUAUACUCCUGGACAGGGAGAUACCAUGAUACGAGAAGUGUUNUCCACAGGGGAGGUCU 60
QY 1 AUAUUAUACUCCUGGACAGGGAGAUACCAUGAUACGAGAAGUGUUNUCCACAGGGGAGGUCU 60
Db 1 AUAUUAUACUCCUGGACAGGGAGAUACCAUGAUACGAGAAGUGUUNUCCACAGGGGAGGUCU 60
QY 61 AUCCAUUUGACUCCGGAUUGUCUGUACCCUCCUGCGAUUUCCCCCAUAUGUGGAGAACTUCGACU 120
Db 61 AUCCAUUUGACUCCGGAUUGUCUGUACCCUCCUCCUGCGAUUUCCCCCAUAUGUGGAGAACTUCGACU 120
QY 61 AUCCAUUUGACUCCGGAUUGUCUGUACCCUCCUCCUGCGAUUUCCCCCAUAUGUGGAGAACTUCGACU 120
Db 61 AUCCAUUUGACUCCGGAUUGUCUGUACCCUCCUCCUGCGAUUUCCCCCAUAUGUGGAGAACTUCGACU 120

QY 121 GCAGAAUUGGCCAU 134
Db 121 GCATTAATTGTGTGT 134

RESULT 5

US-09-621-976-16452
Sequence 16452, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16452
LENGTH: 355
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16452

Query Match 60.5%; Score 127.6; DB 4; Length 355;
Best Local Similarity 73.1%; Pred. No. 6.9e-37;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAACUACCGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 1 ATACTTAACCTGGAGGAGGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 60
QY 61 AUAACUACCGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 120
Db 61 ATACTTAACCTGGAGGAGGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 120
QY 121 GCAGAAUUGGCCAU 134
Db 121 GCATTAATTGTGTGT 134

RESULT 6

US-09-497-855A-32
Sequence 32, Application US/09497855A
Patent No. 6605432
GENERAL INFORMATION:
APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REFERENCE: UMO1523
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/118,760
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 32
LENGTH: 118067
TYPE: DNA
ORGANISM: Homo sapiens;
US-09-497-855A-32

Query Match 60.5%; Score 127.6; DB 4; Length 118067;
Best Local Similarity 73.1%; Pred. No. 9.7e-36;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAACUACCGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 59420 ATACTTAACCTGGAGGAGGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 59479

QY 61 AUAACUACCGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 120
Db 59480 ATACTTAACCTGGAGGAGGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 59539
QY 121 GCAGAAUUGGCCAU 134
Db 59540 GCATTAATTGTGTGT 59553

RESULT 7

US-09-621-976-16458
Sequence 16458, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16458
LENGTH: 204
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16458

Query Match 60.3%; Score 127.2; DB 4; Length 204;
Best Local Similarity 72.4%; Pred. No. 7.5e-37;
Matches 97; Conservative 33; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUAACUACCGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 1 ATACTTAACCTGGAGGAGGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 60
QY 61 AUAACUACCGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 120
Db 61 ATACTTAACCTGGAGGAGGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 120
QY 121 GCAGAAUUGGCCAU 134
Db 121 GCATTAATTGTGTGT 134

RESULT 8

US-09-621-976-16457
Sequence 16457, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16457
LENGTH: 189
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16457

Query Match 59.7%; Score 126; DB 4; Length 189;
Best Local Similarity 72.4%; Pred. No. 2e-36;
Matches 97; Conservative 32; Mismatches 5; Indels 0; Gaps 0;

QY 1 AUAACUACCGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCCAAGGCGAGGCU 60
Db 1 ATACTTAACCTGGAGGAGGAGATACATGATCAGAAAGTGTGTTTCCAGGCGAGGCTT 60

[illegible]

RESULT 2

```

US-10-446-519-1
/ Sequence 1, Application US/10446519
/ Publication No. US2004006039A1
/ GENERAL INFORMATION:
/ APPLICANT: CHATTERJEE, SUBROTO B.
/ TITLE OF INVENTION: A NEUTRAL SPHINGOMYELINASE ANTISENSE RIBOZYME AND USES
/ TITLE OF INVENTION: THEREOP
/ FILE REFERENCE: 58318-CIP (71699)
/ CURRENT APPLICATION NUMBER: US/10/446,519
/ CURRENT FILING DATE: 2003-05-27
/ PRIOR APPLICATION NUMBER: 10/279,215
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: 60/342,631
/ PRIOR FILING DATE: 2001-10-23
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 207
/ TYPE: RNA
/ ORGANISM: Homo sapiens
/ US-10-446-519-1

```

Query Match	73.0%;	Score 154;	DB 16;	Length 207;
Best Local Similarity	87.0%;	Pred. No. 1.2e-44;		
Matches 181; Conservative	0;	Mismatches 25;	Indels 2;	Gaps 1.

[illegible]

RESULT 3

```

US-10-446-519-2/c
; Sequence 2, Application US/10446519
; Publication No. US20040006039A1
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, SUBROTO B.
; TITLE OF INVENTION: A NEUTRAL SPHINGOMYELINASE ANTISENSE RIBOZYME AND USES
; TITLE OF INVENTION: THERIOP
; FILE REFERENCE: 58318-CIP (71699)
; CURRENT APPLICATION NUMBER: US/10/446,519
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: 10/279,215
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/342,631
; PRIOR FILING DATE: 2001-10-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 207

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-519-2

```

Query Match	73.0%;	Score 154;	DB 16;	Length 207;
Best Local Similarity	66.8%;	Pred. No. 1.2e-44;		
Matches 139;	Conservative 42;	Mismatches 25;	Indels 2;	Gaps 1;

[illegible]

RESULT 4

```

US-10-276-302-3
/ Sequence 3, Application US/10276302
/ Publication No. US2003015267A1
GENERAL INFORMATION:
APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
APPLICANT: Murakami, Akihito
APPLICANT: Kojima, Kazuo
TITLE OF INVENTION: Methods and Kits for measuring antibodies against ENA
FILE REFERENCE: P021101
CURRENT APPLICATION NUMBER: US/10/276,302
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: JP P2000-157410
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 164
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Artificially
OTHER INFORMATION: synthesized primer sequence
US-10-276-302-3

```

Query Match	60.5%;	Score 127.6;	DB 15;	Length 164;
Best Local Similarity	73.1%;	Pred. No. 3e-35;		
Matches 98;	Conservative 32;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

RESULT 5

```

US-10-027-632-286819/c
; Sequence 286819, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

```

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286819
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(553)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-286819

```

```

Query Match      60.5%; Score 127.6; DB 13; Length 553;
Best Local Similarity 73.1%; Pred. No. 3.9e-35;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 AUAUCUACUGGAGGAGAGAUACCAUGAUGAGUGUUCUCCAGGCGAGGCUU 60
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      444 ATACTTAACCTGGGAGGAGATACCATGATCAGAAAGTGTTTCCAGGCGAGGCTT 385
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      61 AUCGAUUGCAGUCGCGAGUGUGUACCCCGCGAUAUUCGCAAAUGUGGAAACUGGACU 120
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      384 ATCCATTGCACTCCGATGTGTGACCCCTGCGATTTCGCAATGTGGGAACTGACT 325
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      121 GCAGAAUUGGCGAU 134
         |||:::|:::|:::|
DB      324 GCATAATTGTGTGT 311
         |||:::|:::|:::|

```

```

RESULT 6
US-10-027-632-286819/c
; Sequence 286819, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09

```

```

; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286819
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(553)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-286819

```

```

Query Match      60.5%; Score 127.6; DB 15; Length 553;
Best Local Similarity 73.1%; Pred. No. 3.9e-35;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 AUAUCUACUGGAGGAGAGAUACCAUGAUGAGUGUUCUCCAGGCGAGGCUU 60
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      444 ATACTTAACCTGGGAGGAGATACCATGATCAGAAAGTGTTTCCAGGCGAGGCTT 385
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      61 AUCGAUUGCAGUCGCGAGUGUGUACCCCGCGAUAUUCGCAAAUGUGGAAACUGGACU 120
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      384 ATCCATTGCACTCCGATGTGTGACCCCTGCGATTTCGCAATGTGGGAACTGACT 325
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      121 GCAGAAUUGGCGAU 134
         |||:::|:::|:::|
DB      324 GCATAATTGTGTGT 311
         |||:::|:::|:::|

```

```

RESULT 7
US-10-081-327-32

```

```

; Sequence 32, Application US/10081327
; Publication No. US20030129602A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/10/081,327
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 06/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 06/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 32
; LENGTH: 118067
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-10-081-327-32

```

```

Query Match      60.5%; Score 127.6; DB 15; Length 118067;
Best Local Similarity 73.1%; Pred. No. 1.3e-34;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 AUAUCUACUGGAGGAGAGAUACCAUGAUGAGUGUUCUCCAGGCGAGGCUU 60
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      59420 ATACTTAACCTGGGAGGAGATACCATGATCAGAAAGTGTTTCCAGGCGAGGCTT 59479
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      61 AUCGAUUGCAGUCGCGAGUGUGUACCCCGCGAUAUUCGCAAAUGUGGAAACUGGACU 120
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      59480 ATCCATTGCACTCCGATGTGTGACCCCTGCGATTTCGCAATGTGGGAACTGACT 59539
         |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      121 GCAGAAUUGGCGAU 134
         |||:::|:::|:::|
DB      59540 GCATAATTGTGTGT 59553
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```

```

RESULT 8
US-10-029-386-18128
; Sequence 18128, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:

```

```
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AROMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18128
LENGTH: 167
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR6.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P34318, EVALU8 2.60e+00
OTHER INFORMATION: NT HIT: J00319.1, EVALU8 3.00e-89
US-10-029-386-18128
```

```
Query Match 57.4%; Score 121.2; DB 15; Length 167;
Best Local Similarity 70.9%; Pred. No. 5.8e-33;
Matches 95; Conservative 31; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 AUCACUACCCGAGGAGAGAUACCAUACGAGAGGAGUUUCCAGGCGAGGAGCU 60
Db 4 ATACTTACTCGGAGTGAGATACCATGATCAGGAAGTGTTTCCAGGCGAGGCTT 63
QY 61 AUCACUACCCGAGGAGAGUACCAUACGAGAGGAGUUUCCAGGCGAGGAGCU 120
Db 64 ATCATCGCACTCCGAGATATGTCGACCCGCGATTTTCCCAATGTGGGAACTGACT 123
QY 121 GCAGAAUUGGCGAU 134
Db 124 GCATTAATTGTGTGT 137
```

```
RESULT 9
US-10-029-386-4428
; Sequence 4428, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AROMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4428
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: J00319.1, EVALU8 2.00e-96
; OTHER INFORMATION: EST_HUMAN HIT: A0138351.1, EVALU8 4.00e-70
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US-10-029-386-4428

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Query Match 57.4%; Score 121.2; DB 15; Length 515;
Best Local Similarity 70.9%; Pred. No. 7.5e-33;
Matches 95; Conservative 31; Mismatches 8; Indels 0; Gaps 0;
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```
QY 1 AUCACUACCCGAGGAGAGAUACCAUACGAGAGGAGUUUCCAGGCGAGGAGCU 60
Db 267 ATACTTACTCGGAGTGAGATACCATGATCAGGAAGTGTTTCCAGGCGAGGCTT 326
QY 61 AUCACUACCCGAGGAGAGUACCAUACGAGAGGAGUUUCCAGGCGAGGAGCU 120
Db 327 ATCATCGCACTCCGAGATATGTCGACCCGCGATTTTCCCAATGTGGGAACTGACT 386
QY 121 GCAGAAUUGGCGAU 134
Db 387 GCATTAATTGTGTGT 400
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RESULT 10

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US-10-027-632-32256/C
; Sequence 32256, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32256
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-32256
```

```
Query Match 57.4%; Score 121.2; DB 13; Length 798;
Best Local Similarity 70.9%; Pred. No. 8.2e-33;
Matches 95; Conservative 31; Mismatches 8; Indels 0; Gaps 0;
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```
QY 1 AUCACUACCCGAGGAGAGAUACCAUACGAGAGGAGUUUCCAGGCGAGGAGCU 60
Db 206 ATACTTACTCGGAGTGAGATACCATGATCAGGAAGTGTTTCCAGGCGAGGCTT 147
QY 61 AUCACUACCCGAGGAGAGUACCAUACGAGAGGAGUUUCCAGGCGAGGAGCU 120
Db 146 ATCATCGCACTCCGAGATATGTCGACCCGCGATTTTCCCAATGTGGGAACTGACT 87
QY 121 GCAGAAUUGGCGAU 134
Db 86 GCATTAATTGTGTGT 73
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```
RESULT 11
US-10-027-632-32256/C
; Sequence 32256, Application US/10027632
; Publication No. US20030204075A9
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; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314864
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-314864
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Query Match          54.2%; Score 114.4; DB 13; Length 539;
Best Local Similarity 66.4%; Pred. No. 2e-30;
Matches 89; Conservative 33; Mismatches 12; Indels 0; Gaps 0;
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Qy      1 AUAUCUACCCUGCAGAGGAGAUACCAUGAUCGAGGUGUUUCCAGGCGAGGCU 60
      359 ATACTTAGCTGCGAGAGGAATACCATGATCAAAAGGTGGTTTCCAGGGTGAGGTTT 300
Qy      61 AUCCAUUGCACCUGGAGUGUCUGACCCUGCGAUUUCCCAAUUGUGGAAACUGACU 120
      299 ATCCATTAAACTCAGAGATGCTGACCCCTGCRATTTCCCAAAATGTGGAACTCACT 240
Db      121 GCAGAAUUGCGCAU 134
      239 GCATTAATTGTGAT 226
```

```

RESULT 15
US-10-027-632-79716/c
; Sequence 79716, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79716
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-79716
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Query Match          54.2%; Score 114.4; DB 15; Length 539;
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```

Best Local Similarity 66.4%; Pred. No. 2e-30;
Matches 89; Conservative 33; Mismatches 12; Indels 0; Gaps 0;
Qy      1 AUAUCUACCCUGCAGAGGAGAUACCAUGAUCGAGGUGUUUCCAGGCGAGGCU 60
      359 ATACTTAGCTGCGAGAGGAATACCATGATCAAAAGGTGGTTTCCAGGGTGAGGTTT 300
Db      61 AUCCAUUGCACCUGGAGUGUCUGACCCUGCGAUUUCCCAAUUGUGGAAACUGACU 120
      299 ATCCATTAAACTCAGAGATGCTGACCCCTGCRATTTCCCAAAATGTGGAACTCACT 240
Qy      121 GCAGAAUUGCGCAU 134
      239 GCATTAATTGTGAT 226
```

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Search completed: January 19, 2005, 23:36:58
Job time : 304 secs
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[illegible]

RESULT 2	AL705609	LOCUS	DEFINITION
	AL705609	468 bp	mRNA linear EST 04-SEP-2003
	DKR2p86t2236_r1	686 (synonym: h1cc3)	Homo sapiens cDNA clone
	DKR2p86t2236_5'		mRNA sequence.

ACCESSION	AL705609	
VERSION	AL705609.1	GI:19688964
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (pages 1 to 468)			
Mambute, R., Heudner, D., Mewes, W., Weil, B. and Wiemann, S.)				
Est (Mambute, R., Heudner, D., Mewes, H.W., Weil, B. and Wiemann, S.)				
Unpublished (1999)				
Contact: MIPS				

INGOLTAEDER LANDSTR.1 D-85764 NEUBERG, GERMANY
THIS IS THE 5' SEQUENCE OF THE CLONE INSERT
CLONE FROM S. WIEMANN, MOLECULAR GENOME ANALYSIS, GERMAN CANCER
RESEARCH CENTER (DKFZ); EMAIL s.wiemann@dkfz-heidelberg.de;
SEQUENCED BY AGOWA (BERLIN/GERMANY) WITHIN THE CDNA SEQUENCING
CONSORTIUM OF THE GERMAN GENOME PROJECT.
NO 5A SEQUENCE AVAILABLE.
THIS CLONE (DKFZP686L236) IS AVAILABLE AT THE RZPD IN BERLIN.
PLEASE CONTACT THE RZPD: RESSOURCENZENTRUM, HEUBERWEG 6, 14059
BERLIN-CHARLOTTENBURG, GERMANY; EMAIL: clone@rzpd.de.
LOCATION/QUALIFIERS

```

FEATURES
source
location/Qualifiers
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686L236"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1ib="686 (synonym: hicc3)"
/note="Vector: pTRIPlex2; site_1: SmaI; site_2: SmaI;
cDNA-collection"

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[illegible]

RESULT 3	
BM749651	
LOCUS	556 bp mRNA linear EST 04-MAR-2002
DEFINITION	K-EST0024911 S11SN01 Homo sapiens cDNA S11SN01-4-H10 5', mRNA
ACCESSION	sequence.
	BM749651

VERSION	BM749651.1	GI:19079269
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 556)	
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.	
TITLE	21C Frontier Korean EST Project 2001	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribd.re.kr Plate: 4 row: H column: 10 High quality sequence stop: 556.	

```

FEATURES
SOURCE
    location/Qualifiers
    1. .556
       /organism="Homo sapiens"
       /mol_type="mRNA"
       /db_xref="taxon:9606"
       /clone="S11SNU1-4-H10"
       /sex="M"
       /tissue_type="Stomach"
       /cell_type="Lymphoblast-like"
       /cell_line="SNU-1"
       /lab_host="TOP10F"
       /clone_1b="S11SNU1"
       /note="Organ: Stomach; Vector: pME18-Fl3; Site 1: XhoI;
       Site 2: XhoI. The poly (A) + RNA was dephosphorylated with
       bacterial alkaline phosphatase (BAP) and then decapped
       with tobacco acid pyrophosphatase (TAP). The decapped
       intact mRNA was ligated with DNA-RNA linker including SfiII
       site by treatment of T4 RNA ligase and the first strand
       cDNA was synthesized with Superscript II using SfiI
       oligo-dT primer. After first strand synthesis, RNA was
       degraded by NaOH treatment and cDNA was amplified by PCR
       reaction. The PCR products were digested with SfiI and
       cloned into DraIII- digested pMB185-Fl3 vector. The
       obtained cDNA vectors were used for transformation of
       competent cells B. coli Top10F by electroporation method.
       The cDNA libraries constructed by this method are
       full-length enriched cDNA library."

```

[illegible]

RESULT 4	
BP455568	
LOCUS	565 bp mRNA linear EST 31-DEC-2003
DEFINITION	BP455568 full-length enriched swine cDNA library, adult ovary Sus
DEFINITION	scrofa cDNA clone OVRM10152B01 5', mRNA sequence.
ACCESSION	BP455568

VERSION BP455568.1 GI:40466788
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa (pig)
 REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 AUTHORS Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T.
 TITLE PEDF (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
 JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
 COMMENT Contact: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.
 FEATURES
 source
 1. 565
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="OVRM10152B01"
 /tissue_type="ovary"
 /dev_stage="adult"
 /clone_1lb="full-length enriched swine cDNA library, adult ovary"
 ORIGIN
 Query Match 60.5%; Score 127.6; DB 5; Length 565;
 Best Local Similarity 73.1%; Pred. No. 1.5e-29;
 Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AUAUCUACCCUGGAGGAGAGAUCCAUAGUACGAAAGUGUUUCCAGAGGCGAGGCUU 60
 Db 1 ATACTTACTCTGGAGGAGATACATGATCAGAAAGTGTGTTCCAGAGGCGAGGCTT 60
 QY 61 AUCCAUUGACUCCGGAUGUGUGUAGCCCGGGAUUNUCCCAAUUGGGAAACUGGACU 120
 Db 61 ATCATTTGACCTCGGATGTGTGACCCCTGCGATTTCCTCCAAATGTGGAAACTGCAT 120
 QY 121 GCAGAAUUGGCGCAU 134
 Db 121 GCATTAATTGTGTGT 134
 RESULT 5
 CBI23444 567 bp mRNA linear EST 29-JAN-2003
 LOCUS K-ESF011806 L13SNU387 Homo sapiens cDNA clone L13SNU387-4-E11 5',
 DEFINITION mRNA sequence.
 ACCESSION CBI23444
 VERSION CBI23444.1 GI:28082873
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoan-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongseung@mail.krbb.re.kr
 Plate: 4 row: E column: 11
 High quality sequence stop: 567.
 FEATURES
 source
 1. 567
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L13SNU387-4-E11"
 /sex="F"
 /tissue_type="liver"
 /cell_line="Epithelial"
 /lab_host="Top10F"
 /clone_1lb="L13SNU387"
 /note="Organ: Liver; Vector: PCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
 ORIGIN
 Query Match 60.5%; Score 127.6; DB 6; Length 567;
 Best Local Similarity 73.1%; Pred. No. 1.5e-29;
 Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AUAUCUACCCUGGAGGAGAGAUCCAUAGUACGAAAGUGUUUCCAGAGGCGAGGCUU 60
 Db 1 ATACTTACTCTGGAGGAGATACATGATCAGAAAGTGTGTTCCAGAGGCGAGGCTT 60
 QY 61 AUCCAUUGACUCCGGAUGUGUGUAGCCCGGGAUUNUCCCAAUUGGGAAACUGGACU 120
 Db 61 ATCATTTGACCTCGGATGTGTGACCCCTGCGATTTCCTCCAAATGTGGAAACTGCAT 120
 QY 121 GCAGAAUUGGCGCAU 134
 Db 121 GCATTAATTGTGTGT 134
 RESULT 6
 BP452975 602 bp mRNA linear EST 30-DEC-2003
 LOCUS BP452975
 DEFINITION BP452975 full-length enriched swine cDNA library, adult liver Sus
 ACCESSION BP452975
 VERSION BP452975.1 GI:40443042
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa (pig)
 REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 AUTHORS Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamasima, N. and Awata, T.
 TITLE PEDF (Pig EST Data Explorer): construction of a database for ESTs

JOURNAL
COMMENT

derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)

Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627

Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute

Single pass sequencing of clones derived from oligo-capped cDNA
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319

Low quality bases were trimmed based on the quality values.

FEATURES

Source

Location/Qualifiers
1..602
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="LVRM10159F12"
/tissue_type="liver"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
liver"

ORIGIN

Query Match 60.5%; Score 127.6; DB 5; Length 602;
Best Local Similarity 73.1%; Pred. No. 1.6e-29;

Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUNCUUACCCUGGAGGAGGAGUACCAAGACGAGAGUGUUUCCAGGGCGAGGCTU 60

Db 1 ATACTTACCTGGGAGGAGATACCAAGATCACGAGAGTGATTTTCCAGGCGAGGCTT 60

QY 61 AUCCAUUGCAGUCGAGUGUGUGACCCGUGCGAUUUUCCCAAUUGGGAACUCGACU 120

Db 61 ATCCATTGCACTCCGATGTGCTGACCCCTGCGATTTCCTCCCAATGTGGAAACTCGACT 120

QY 121 GCAGAAUUGGCGAU 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

QY 121 GCATAATTGTGTGT 134

Db 121 GCATAATTGTGTGT 134

SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CHUARG08"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is
cloned randomly with the EcoRI digestion"

ORIGIN

Query Match 60.5%; Score 127.6; DB 1; Length 614;
Best Local Similarity 73.1%; Pred. No. 1.6e-29;

Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

QY 1 AUNCUUACCCUGGAGGAGGAGUACCAAGACGAGAGUGUUUCCAGGGCGAGGCTU 60

Db 62 ATACTTACCTGGGAGGAGATACCAAGATCACGAGAGTGATTTTCCAGGGCGAGGCTT 121

QY 61 AUCCAUUGCAGUCGAGUGUGUGACCCGUGCGAUUUUCCCAAUUGGGAACUCGACU 120

Db 122 ATCCATTGCACTCCGATGTGCTGACCCCTGCGATTTCCTCCCAATGTGGAAACTCGACT 181

QY 121 GCAGAAUUGGCGAU 134

Db 182 GCATAATTGTGTGT 195

QY 182 GCATAATTGTGTGT 195

Db 182 GCATAATTGTGTGT 195

QY 182 GCATAATTGTGTGT 195

Db 182 GCATAATTGTGTGT 195

QY 182 GCATAATTGTGTGT 195

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QY 182 GCATAATTGTGTGT 195

ORIGIN

Query Match 60.5%; Score 127.6; DB 1; Length 620;
Best Local Similarity 73.1%; Pred. No. 1.6e-29;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1008378"
/tissue_type="placenta"
/clone_lib="PLACE1"
/note="Vector: pME18SFL3"

JOURNAL
COMMENT

HELIX RESEARCH INSTITUTE
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute, cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

Source

1..620
/organism="Homo sapiens"
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/tissue_type="placenta"
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Query Match 60.5%; Score 127.6; DB 1; Length 620;
Best Local Similarity 73.1%; Pred. No. 1.6e-29;
Matches 98; Conservative 32; Mismatches 4; Indels 0; Gaps 0;

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QY 121 GCAGAAUUGGCGCAU 134
Db 121 GCATAATTGTGTGT 134

RESULT 9
CE201300/c 715 bp DNA linear GSS 25-SEP-2003
LOCUS tigr-gss-dog-17000372228685 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE201300
VERSION CE201300.1 GI:35356955
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE Bukaryova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Kirness,E.F., Balne,V., Halpern,A.L., Levy,S., Remington,K.,
Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirness@tigr.org
Class: shotgun.

FEATURES
source Location/Qualifiers
1..715
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: Bacti; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 60.5%; Score 127.6; DB 9; Length 715;
Best Local Similarity 73.1%; Pred. No. 1.6e-29; Indels 0; Gaps 0;
Matches 98; Conservative 32; Mismatches 4;

QY 1 AUAUACCUAGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCAGAGGAGGAGCU 60
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QY 61 AUCCAUUGCAGUCUGGAGUUGUGUGUACCCUGCGAUUUCCCCAAUUGUGGAAACUCGACU 120
Db 269 ATCCATTGACCTCGGATGTGCTGACCCCTCGCATTTCCCAATGTGGGAAACTCGACT 210
QY 121 GCAGAAUUGGCGCAU 134
Db 209 GCATAATTGTGTGT 196

RESULT 10
BP147290 742 bp mRNA linear EST 30-DEC-2003
LOCUS BP147290

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DEFINITION BP147290 full-length enriched swine cDNA library, adult ovary Sus
scrofa cDNA clone OVRM10127811 5', mRNA sequence.
ACCESSION BP147290
VERSION BP147290.1 GI:40396761
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE Bukaryova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 742)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.
PEDB (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
COMMENT Contact: Hirohide Uenishi
National Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STRAF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES
source Location/Qualifiers
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/organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="OVRM10127811"
/cisue_type="ovary"
/dev_stage="adult"
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ORIGIN
Query Match 60.5%; Score 127.6; DB 5; Length 742;
Best Local Similarity 73.1%; Pred. No. 1.6e-29; Indels 0; Gaps 0;
Matches 98; Conservative 32; Mismatches 4;

QY 1 AUAUACCUAGGAGGAGAGAUACAUGAUCAGAAAGUGUUUCCAGAGGAGGAGCU 60
Db 1 ATACTTACCTGGAGGAGAGATACATGATCAGAAAGTGTGTTTCCAGAGGAGGCTT 60
QY 61 AUCCAUUGCAGUCUGGAGUUGUGUGUACCCUGCGAUUUCCCCAAUUGUGGAAACUCGACU 120
Db 61 ATCCATTGACCTCGGATGTGCTGACCCCTCGCATTTCCCAATGTGGGAAACTCGACT 120
QY 121 GCAGAAUUGGCGCAU 134
Db 121 GCATAATTGTGTGT 134

RESULT 11
BP437373 781 bp mRNA linear EST 30-DEC-2003
LOCUS BP437373
DEFINITION BP437373 full-length enriched swine cDNA library, adult lung Sus
scrofa cDNA clone LING010036E06 5', mRNA sequence.
ACCESSION BP437373
VERSION BP437373.1 GI:40427440
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE Bukaryova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 781)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,

```

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Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishl@affrc.go.jp


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OY      61  AUCGCAUUGGACUCGCGGGAUUGUCGACCCUUGCGAUUCCCCCAAUUGUGGAAACUCGACU 120
      Db      61  ATCCATTGCACTCCGGAATGTGTGACCCCTCGGATTTCCCAATGTGGGAACTCGACT 120
OY      121  GCAGAAUUGGCGAU 134
      Db      121  GCATTAATTGTGGT 134
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Job time : 1842 secs